SEQUENCE LISTING

<110> Degussa AG

<120> Process for preparing optically active amino acids using a whole-cell catalyst

<130> 040055 AM

<160> 13

<170> PatentIn version 3.1

<210> 1
<211> 47
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 1
aaaaaactta agaaggagat atacatatga cattagaaat cttcgaa   47

<210> 2
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 2
aaaaaactgc agttagcgac ggctaataat at   32

<210> 3
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 3
aaaaaacata tgaagattgt cttagttctt   30

<210> 4
<211> 32
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 4
aaaaaagacg tcttatttct tatcgtgttt ac   32

```
<210>   5
<211>   1120
<212>   DNA
<213>   Bacillus cereus

<220>
<221>   CDS
<222>   (20)..(1120)
<223>

<400>   5
ttaagaagga gatatacat atg aca tta gaa atc ttc gaa tac tta gaa aaa        52
                     Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys
                     1               5                   10

tat gat tat gag caa gta gta ttt tgt caa gat aaa gaa tct ggt tta       100
Tyr Asp Tyr Glu Gln Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu
            15                  20                  25

aaa gca att att gca att cat gat aca aca ctt gga ccg gct ctt ggt       148
Lys Ala Ile Ile Ala Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly
        30                  35                  40

gga aca aga atg tgg aca tat gat tct gaa gaa gcg gcg att gaa gat       196
Gly Thr Arg Met Trp Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp
        45                  50                  55

gca ttg cgt ctt gca aaa ggg atg aca tac aaa aac gca gca gct ggt       244
Ala Leu Arg Leu Ala Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly
60                  65                  70                  75

tta aac tta ggt ggt gcg aaa aca gta att atc ggt gat cct cgt aaa       292
Leu Asn Leu Gly Gly Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys
                80                  85                  90

gat aag agc gaa gca atg ttc cgt gca cta gga cgt tat atc caa gga       340
Asp Lys Ser Glu Ala Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly
            95                  100                 105

cta aac gga cgt tac att aca gct gaa gat gtt ggt aca aca gta gat       388
Leu Asn Gly Arg Tyr Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp
        110                 115                 120

gat atg gat att atc cat gaa gaa act gac ttt gta aca ggt atc tca       436
Asp Met Asp Ile Ile His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser
        125                 130                 135

cca tca ttc ggt tct tct ggt aac cca tct ccg gta act gca tac ggt       484
Pro Ser Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly
140                 145                 150                 155

gtt tac cgt ggt atg aaa gca gct gca aaa gaa gct ttc ggt act gac       532
Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp
                160                 165                 170

aat tta gaa gga aaa gta att gct gtt caa ggc gtt ggt aac gta gca       580
Asn Leu Glu Gly Lys Val Ile Ala Val Gln Gly Val Gly Asn Val Ala
```

```
                    175                    180                    185

      tat cac cta tgc aaa cat tta cac gct gaa gga gca aaa tta att gtt    628
      Tyr His Leu Cys Lys His Leu His Ala Glu Gly Ala Lys Leu Ile Val
  5           190                195                200

      aca gat att aat aaa gaa gct gta caa cgt gct gta gaa gaa ttc ggt    676
      Thr Asp Ile Asn Lys Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly
              205                210                215
 10
      gca tca gca gtt gaa cca aat gaa att tac ggt gtt gaa tgc gat att    724
      Ala Ser Ala Val Glu Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile
      220                225                230                235

 15   tac gca cca tgt gca cta ggc gca aca gtt aat gat gaa act att cca    772
      Tyr Ala Pro Cys Ala Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro
                  240                245                250

      caa ctt aaa gca aaa gta atc gca ggt tct gcg aat aac caa tta aaa    820
 20   Gln Leu Lys Ala Lys Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys
                  255                260                265

      gaa gat cgt cat ggt gac atc att cat gaa atg ggt att gta tac gca    868
      Glu Asp Arg His Gly Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala
 25           270                275                280

      cca gat tat gta att aat gca ggt ggc gta att aac gta gca gac gaa    916
      Pro Asp Tyr Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu
              285                290                295
 30
      tta tat gga tac aat aga gaa cgt gca cta aaa cgt gtt gag tct att    964
      Leu Tyr Gly Tyr Asn Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile
      300                305                310                315

 35   tat gac acg att gca aaa gta atc gaa att tca aaa cgc gat ggc ata   1012
      Tyr Asp Thr Ile Ala Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile
                  320                325                330

      gca act tat gta gcg gca gat cgt cta gct gaa gag cgc att gca agc   1060
 40   Ala Thr Tyr Val Ala Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser
                  335                340                345

      ttg aag aat tct cgt agc act tac tta cgc aac ggt cac gat att att   1108
      Leu Lys Asn Ser Arg Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile
 45           350                355                360

      agc cgt cgc taa                                                   1120
      Ser Arg Arg
              365
 50

      <210>  6
      <211>  366
      <212>  PRT
 55   <213>  Bacillus cereus

      <400>  6

      Met Thr Leu Glu Ile Phe Glu Tyr Leu Glu Lys Tyr Asp Tyr Glu Gln
```

```
         1                    5                        10                       15

 5       Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu Lys Ala Ile Ile Ala
                     20              25                  30

         Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly Gly Thr Arg Met Trp
10                   35              40                  45

         Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp Ala Leu Arg Leu Ala
                 50              55              60

15       Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly Leu Asn Leu Gly Gly
         65              70              75                      80

20   Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys Asp Lys Ser Glu Ala
                     85                  90                  95

         Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly Leu Asn Gly Arg Tyr
25                   100             105                 110

         Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp Asp Met Asp Ile Ile
                 115             120                 125
30
         His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser Pro Ser Phe Gly Ser
                 130             135                 140

35       Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met
         145             150                 155                 160

40       Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys
                         165             170                 175

         Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys
45                   180             185                 190

         His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys
                 195             200                 205
50
         Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu
                 210             215                 220

55       Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala
         225             230                 235                 240
```

```
        Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys
                        245             250             255

  5     Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly
                        260             265             270

        Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile
 10                 275             280             285

        Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn
                    290             295             300
 15

        Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala
        305              310             315                 320

 20
        Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala
                        325             330             335

 25     Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser Leu Lys Asn Ser Arg
                    340             345             350

        Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg
 30             355             360             365


        <210>   7
        <211>   1095
 35     <212>   DNA
        <213>   Candida boidinii

        <220>
        <221>   CDS
 40     <222>   (1)..(1095)
        <223>

        <400>   7
        atg aag att gtc tta gtt ctt tat gat gct ggt aag cac gct gct gat        48
 45     Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
        1               5               10              15

        gaa gaa aaa tta tat ggt tct act gaa aat aaa tta ggt att gct aat        96
        Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn
 50                     20              25              30

        tgg tta aaa gat caa ggt cat gaa cta att act act tct gat aaa gaa       144
        Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
                        35              40              45
 55
        ggt gaa aca agt gaa ttg gat aaa cat atc cca gat gct gat att atc       192
        Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile
                    50              55              60
```

```
       atc acc act cct ttc cat cct gct tat atc act aag gaa aga ctt gac    240
       Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
       65              70              75                  80

    5  aag gct aag aac tta aaa tta gtc gtt gtc gct ggt gtt ggt tct gat    288
       Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
                       85              90              95

       cac att gat tta gat tat att aat caa aca ggt aag aaa atc tca gtc    336
   10  His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
                       100             105             110

       ctg gaa gtt aca ggt tct aat gtt gtc tct gtt gct gaa cac gtt gtc    384
   15  Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
                   115             120             125

       atg acc atg ctt gtc ttg gtt aga aat ttc gtt cca gca cat gaa caa    432
       Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
           130             135             140
   20
       att att aac cac gat tgg gag gtt gct gct atc gct aag gat gct tac    480
       Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
       145             150             155             160

   25  gat atc gaa ggt aaa act atc gct acc att ggt gct ggt aga att ggt    528
       Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
                       165             170             175

       tac aga gtc ttg gaa aga tta ctc cca ttt aat cca aaa gaa tta tta    576
   30  Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu
                   180             185             190

       tac tac gat tat caa gct tta cca aaa gaa gct gaa gaa aaa gtt ggt    624
       Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly
   35          195             200             205

       gct aga aga gtt gaa aat att gaa gaa tta gtt gct caa gct gat atc    672
       Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile
               210             215             220
   40
       gtt aca gtt aat gct cca tta cac gca ggt aca aaa ggt tta att aat    720
       Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
       225             230             235             240

   45  aag gaa tta tta tct aaa ttt aaa aaa ggt gct tgg tta gtc aat acc    768
       Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr
                       245             250             255

       gca aga ggt gct att gct gtt gct gaa gat gtt gca gca gct tta gaa    816
   50  Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu
                       260             265             270

       tct ggt caa tta aga ggt tac ggt ggt gat gtt tgg ttc cca caa cca    864
       Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
   55              275             280             285

       gct cca aag gat cac cca tgg aga gat atg aga aat aaa tat ggt gct    912
       Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
               290             295             300
```

```
ggt aat gcc atg act cct cac tac tct ggt act act tta gac gct caa          960
Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln
305                 310                 315                 320

aca aga tac gct gaa ggt act aaa aat att ttg gaa tca ttc ttt acc        1008
Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr
                325                 330                 335

ggt aaa ttt gat tac aga cca caa gat att atc tta tta aat ggt gaa        1056
Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu
                340                 345                 350

tac gtt act aaa gct tac ggt aaa cac gat aag aaa taa                    1095
Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
            355                 360
```

```
<210>  8
<211>  364
<212>  PRT
<213>  Candida boidinii

<400>  8

Met Lys Ile Val Leu Val Leu Tyr Asp Ala Gly Lys His Ala Ala Asp
1               5               10                  15

Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn
            20                  25                  30

Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu
        35                  40                  45

Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile
    50                  55                  60

Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp
65                  70                  75                  80

Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp
                85                  90                  95

His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val
                100                 105                 110

Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val
            115                 120                 125

Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln
        130                 135                 140
```

```
         Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr
   5     145             150             155             160

         Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly
                         165             170             175
  10

         Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu
                     180             185             190

  15     Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly
                     195             200             205

         Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile
  20         210             215             220

         Val Thr Val Asn Ala Pro Leu His Ala Gly Thr Lys Gly Leu Ile Asn
         225             230             235             240
  25

         Lys Glu Leu Leu Ser Lys Phe Lys Lys Gly Ala Trp Leu Val Asn Thr
                         245             250             255

  30
         Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu
                         260             265             270

  35     Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro
                     275             280             285

         Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala
  40         290             295             300

         Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln
         305             310             315             320
  45

         Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr
                     325             330             335

  50
         Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu
                     340             345             350

  55     Tyr Val Thr Lys Ala Tyr Gly Lys His Asp Lys Lys
                     355             360
```

<210>   9

```
<211>  5686
<212>  DNA
<213>  Artificial

<220>
<223>  Plasmid pAM3.25

<400>  9
tatgaagatt gtcttagttc tttatgatgc tggtaagcac gctgctgatg aagaaaaatt      60

atatggttct actgaaaata aattaggtat tgctaattgg ttaaaagatc aaggtcatga     120

actaattact acttctgata agaaggtga aacaagtgaa ttggataaac atatcccaga      180

tgctgatatt atcatcacca ctcctttcca tcctgcttat atcactaagg aaagacttga     240

caaggctaag aacttaaaat tagtcgttgt cgctggtgtt ggttctgatc acattgattt     300

agattatatt aatcaaacag gtaagaaaat ctcagtcctg gaagttacag gttctaatgt     360

tgtctctgtt gctgaacacg ttgtcatgac catgcttgtc ttggttagaa atttcgttcc     420

agcacatgaa caaattatta accacgattg ggaggttgct gctatcgcta aggatgctta     480

cgatatcgaa ggtaaaacta tcgctaccat tggtgctggt agaattggtt acagagtctt     540

ggaaagatta ctcccattta atccaaaaga attattatac tacgattatc aagctttacc     600

aaaagaagct gaagaaaag ttggtgctag aagagttgaa atattgaag aattagttgc      660

tcaagctgat atcgttacag ttaatgctcc attacacgca ggtacaaaag gtttaattaa     720

taaggaatta ttatctaaat ttaaaaaagg tgcttggtta gtcaataccg caagaggtgc     780

tattgctgtt gctgaagatg ttgcagcagc tttagaatct ggtcaattaa gaggttacgg     840

tggtgatgtt tggttcccac aaccagctcc aaaggatcac ccatggagag atatgagaaa     900

taaatatggt gctggtaatg ccatgactcc tcactactct ggtactactt tagacgctca     960

aacaagatac gctgaaggta ctaaaaatat tttggaatca ttctttaccg gtaaatttga    1020

ttacagacca caagatatta tcttattaaa tggtgaatac gttactaaag cttacggtaa    1080

acacgataag aaataagacg tcaagcttgg ctgttttggc ggatgagaga agattttcag    1140

cctgatacag attaaatcag aacgcagaag cggtctgata aaacagaatt gcctggcgg     1200

cagtagcgcg gtggtcccac ctgaccccat gccgaactca gaagtgaaac gccgtagcgc    1260

cgatggtagt gtggggtctc cccatgcgag agtagggaac tgccaggcat caaataaaac    1320

gaaaggctca gtcgaaagac tgggcctttc gttttatctg ttgtttgtcg gtgaacgctc    1380

tcctgagtag acaaatccg ccgggagcgg atttgaacgt tgcgaagcaa cggcccggag     1440

ggtggcgggc aggacgcccg ccataaactg ccaggcatca aattaagcag aaggccatcc    1500

tgacggatgg cctttttgcg tttctacaaa ctcttttgtt tattttttcta aatacattca    1560
```

```
aatatgtatc cgctcatgag acaataaccc tgataaatgc ttcaataata ttgaaaaagg    1620

aagagtatga gtattcaaca tttccgtgtc gcccttattc ccttttttgc ggcattttgc    1680

cttcctgttt ttgctcaccc agaaacgctg gtgaaagtaa aagatgctga agatcagttg    1740

ggtgcacgag tgggttacat cgaactggat ctcaacagcg gtaagatcct tgagagtttt    1800

cgccccgaag aacgttttcc aatgatgagc actttaaag ttctgctatg tggcgcggta    1860

ttatcccgtg ttgacgccgg gcaagagcaa ctcggtcgcc gcatacacta ttctcagaat    1920

gacttggttg agtactcacc agtcacagaa aagcatctta cggatggcat gacagtaaga    1980

gaattatgca gtgctgccat aaccatgagt gataacactg cggccaactt acttctgaca    2040

acgatcggag gaccgaagga gctaaccgct tttttgcaca acatggggga tcatgtaact    2100

cgccttgatc gttgggaacc ggagctgaat gaagccatac caaacgacga gcgtgacacc    2160

acgatgcctg tagcaatggc aacaacgttg cgcaaactat taactggcga actacttact    2220

ctagcttccc ggcaacaatt aatagactgg atggaggcgg ataaagttgc aggaccactt    2280

ctgcgctcgg cccttccggc tggctggttt attgctgata atctggagc cggtgagcgt     2340

gggtctcgcg gtatcattgc agcactgggg ccagatggta agccctcccg tatcgtagtt    2400

atctacacga cggggagtca ggcaactatg gatgaacgaa atagacagat cgctgagata    2460

ggtgcctcac tgattaagca ttggtaactg tcagaccaag tttactcata tatactttag    2520

attgatttaa aacttcattt ttaatttaaa aggatctagg tgaagatcct ttttgataat    2580

ctcatgacca aaatccctta acgtgagttt tcgttccact gagcgtcaga ccccgtagaa    2640

aagatcaaag gatcttcttg agatcctttt tttctgcgcg taatctgctg cttgcaaaca    2700

aaaaaccac cgctaccagc ggtggtttgt ttgccggatc aagagctacc aactcttttt     2760

ccgaaggtaa ctggcttcag cagagcgcag ataccaaata ctgtccttct agtgtagccg    2820

tagttaggcc accacttcaa gaactctgta gcaccgccta catacctcgc tctgctaatc    2880

ctgttaccag tggctgctgc cagtggcgat aagtcgtgtc ttaccgggtt ggactcaaga    2940

cgatagttac cggataaggc gcagcggtcg gctgaacgg ggggttcgtg cacacagccc     3000

agcttggagc gaacgaccta caccgaactg agatacctac agcgtgagct atgagaaagc    3060

gccacgcttc ccgaagggag aaaggcggac aggtatccgg taagcggcag ggtcggaaca    3120

ggagagcgca cgagggagct ccaggggga aacgcctggt atctttatag tcctgtcggg     3180

tttcgccacc tctgacttga gcgtcgattt ttgtgatgct cgtcagggg gcggagccta     3240

tggaaaaacg ccagcaacgc ggccttttta cggttcctgg cctttgctg gccttttgct     3300
```

```
cacatgttct ttcctgcgtt atcccctgat tctgtggata accgtattac cgcctttgag    3360

tgagctgata ccgctcgccg cagccgaacg accgagcgca gcgagtcagt gagcgaggaa    3420

gcggaagagc gcctgatgcg gtattttctc cttacgcatc tgtgcggtat ttcacaccgc    3480

atatatggtg cactctcagt acaatctgct ctgatgccgc atagttaagc cagtatacac    3540

tccgctatcg ctacgtgact gggtcatggc tgcgccccga cacccgccaa cacccgctga    3600

cgcgccctga cgggcttgtc tgctcccggc atccgcttac agacaagctg tgaccgtctc    3660

cgggagctgc atgtgtcaga ggttttcacc gtcatcaccg aaacgcgcga ggcagctgcg    3720

gtaaagctca tcagcgtggt cgtgaagcga ttcacagatg tctgcctgtt catccgcgtc    3780

cagctcgttg agtttctcca gaagcgttaa tgtctggctt ctgataaagc gggccatgtt    3840

aagggcggtt ttttcctgtt tggtcacttg atgcctccgt gtaaggggga atttctgttc    3900

atggggtaa tgataccgat gaaacgagag aggatgctca cgatacgggt tactgatgat    3960

gaacatgccc ggttactgga acgttgtgag ggtaaacaac tggcggtatg gatgcggcgg    4020

gaccagagaa aaatcactca gggtcaatgc cagcgcttcg ttaatacaga tgtaggtgtt    4080

ccacagggta gccagcagca tcctgcgatg cagatccgga acataatggt gcagggcgct    4140

gacttccgcg tttccagact ttacgaaaca cggaaaccga agaccattca tgttgttgct    4200

caggtcgcag acgttttgca gcagcagtcg cttcacgttc gctcgcgtat cggtgattca    4260

ttctgctaac cagtaaggca accccgccag cctagccggg tcctcaacga caggagcacg    4320

atcatgcgca cccgtggcca ggacccaacg ctgcccgaga tgcgccgcgt gcggctgctg    4380

gagatggcgg acgcgatgga tatgttctgc caagggttgg tttgcgcatt cacagttctc    4440

cgcaagaatt gattggctcc aattcttgga gtggtgaatc cgttagcgag gtgccgccgg    4500

cttccattca ggtcgaggtg gcccggctcc atgcaccgcg acgcaacgcg gggaggcaga    4560

caaggtatag ggcggcgcct acaatccatg ccaacccgtt ccatgtgctc gccgaggcgg    4620

cataaatcgc cgtgacgatc agcggtccag tgatcgaagt taggctggta agagccgcga    4680

gcgatccttg aagctgtccc tgatggtcgt catctacctg cctggacagc atggcctgca    4740

acgcgggcat cccgatgccg ccggaagcga agaatcat aatggggaag gccatccagc     4800

ctcgcgtcgc gaacgccagc aagacgtagc ccagcgcgtc ggccgccatg ccggcgataa    4860

tggcctgctt ctcgccgaaa cgtttggtgg cgggaccagt gacgaaggct tgagcgaggg    4920

cgtgcaagat tccgaatacc gcaagcgaca ggccgatcat cgtcgcgctc cagcgaaagc    4980

ggtcctcgcc gaaaatgacc cagagcgctg ccggcacctg tcctacgagt tgcatgataa    5040

agaagacagt cataagtgcg gcgacgatag tcatgccccg cgcccaccgg aaggagctga    5100
```

```
        ctgggttgaa ggctctcaag ggcatcggtc gacgctctcc cttatgcgac tcctgcatta      5160

        ggaagcagcc cagtagtagg ttgaggccgt tgagcaccgc cgccgcaagg aatggtgcat      5220

        gctcgatggc tacgagggca gacagtaagt ggatttacca taatccctta attgtacgca      5280

        ccgctaaaac gcgttcagcg cgatcacggc agcagacagg taaaaatggc aacaaaccac      5340

        cctaaaaact gcgcgatcgc gcctgataaa ttttaaccgt atgaatacct atgcaaccag      5400

        agggtacagg ccacattacc cccacttaat ccactgaagc tgccattttt catggtttca      5460

        ccatcccagc gaagggccat gcatgcatcg aaattaatac gacgaaatta atacgactca      5520

        ctatagggca attgcgatca ccacaattca gcaaattgtg aacatcatca cgttcatctt      5580

        tccctggttg ccaatggccc attttcctgt cagtaacgag aaggtcgcga attcaggcgc      5640

        tttttagact ggtcgtaatg aacaattctt aagaaggaga tataca                    5686


        <210>  10
        <211>  5106
        <212>  DNA
        <213>  Artificial

        <220>
        <223>  Plasmid pAM10.1

        <400>  10
        gaaggagata tacatatgac attagaaatc ttcgaatact tagaaaaata tgattatgag       60

        caagtagtat tttgtcaaga taaagaatct ggtttaaaag caattattgc aattcatgat      120

        acaacacttg gaccggctct ggtggaaca agaatgtgga catatgattc tgaagaagcg      180

        gcgattgaag atgcattgcg tcttgcaaaa gggatgacat acaaaaacgc agcagctggt      240

        ttaaacttag gtggtgcgaa aacagtaatt atcggtgatc ctcgtaaaga taagagcgaa      300

        gcaatgttcc gtgcactagg acgttatatc caaggactaa acggacgtta cattacagct      360

        gaagatgttg gtacaacagt agatgatatg gatattatcc atgaagaaac tgactttgta      420

        acaggtatct caccatcatt cggttcttct ggtaacccat ctccggtaac tgcatacggt      480

        gtttaccgtg gtatgaaagc agctgcaaaa gaagctttcg gtactgacaa tttagaagga      540

        aaagtaattg ctgttcaagg cgttggtaac gtagcatatc acctatgcaa acatttacac      600

        gctgaaggag caaaattaat tgttacagat attaataaag aagctgtaca acgtgctgta      660

        gaagaattcg gtgcatcagc agttgaacca aatgaaattt acggtgttga atgcgatatt      720

        tacgcaccat gtgcactagg cgcaacagtt aatgatgaaa ctattccaca acttaaagca      780

        aaagtaatcg caggttctgc gaataaccaa ttaaagaag atcgtcatgg tgacatcatt      840
```

```
catgaaatgg gtattgtata cgcaccagat tatgtaatta atgcaggtgg cgtaattaac      900

gtagcagacg aattatatgg atacaataga gaacgtgcac taaaacgtgt tgagtctatt      960

tatgacacga ttgcaaaagt aatcgaaatt tcaaaacgcg atggcatagc aacttatgta     1020

gcggcagatc gtctagctga agagcgcatt gcaagcttga agaattctcg tagcacttac     1080

ttacgcaacg gtcacgatat tattagccgt cgctaacgcg tttgcggttg caaaatggc      1140

gcagcagcaa ggcgtggcgg tgaaaacctc tgccgaagcc ctgcaacagg ccattgacga     1200

taatttctgg caagccgaat accgcgacta ccgccgtacc tccatctaaa agcttatcga     1260

tgataagctg tcaaacatga gaattacaac ttatatcgta tggggctgac ttcaggtgct     1320

acatttgaag agataaattg cactgaaatc tagaaatatt ttatctgatt aataagatga     1380

tcttcttgag atcgttttgg tctgcgcgta atctcttgct ctgaaaacga aaaaaccgcc     1440

ttgcagggcg gttttttcgaa ggttctctga gctaccaact ctttgaaccg aggtaactgg    1500

cttggaggag cgcagtcacc aaaacttgtc ctttcagttt agccttaacc ggcgcatgac     1560

ttcaagacta actcctctaa atcaattacc agtggctgct gccagtggtg cttttgcatg     1620

tctttccggg ttggactcaa gacgatagtt accggataag gcgcagcggt cggactgaac     1680

ggggggttcg tgcatacagt ccagcttgga gcgaactgcc tacccggaac tgagtgtcag     1740

gcgtggaatg agacaaacgc ggccataaca gcggaatgac accggtaaac cgaaaggcag     1800

gaacaggaga gcgcacgagg gagccgccag gggaaacgcc tggtatcttt atagtcctgt     1860

cgggtttcgc caccactgat ttgagcgtca gatttcgtga tgcttgtcag ggggcggag      1920

cctatggaaa aacggctttg ccgcggccct ctcacttccc tgttaagtat cttcctggca     1980

tcttccagga aatctccgcc ccgttcgtaa gccatttccg ctcgccgcag tcgaacgacc     2040

gagcgtagcg agtcagtgag cgaggaagcg gaatatatcc tgtatcacat attctgctga     2100

cgcaccggtg cagccttttt tctcctgcca catgaagcac ttcactgaca ccctcatcag     2160

tgccaacata gtaagccagt atacactccg ctagcgctga tgtccggcgg tgcttttgcc     2220

gttacgcacc accccgtcag tagctgaaca ggagggacag ctgatagaaa cagaagccac     2280

tggagcacct caaaaacacc atcatacact aaatcagtaa gttggcagca tcacccgacg     2340

cactttgcgc cgaataaata cctgtgacgg aagatcactt cgcagaataa ataaatcctg     2400

gtgtccctgt tgataccggg aagccctggg ccaacttttg cgaaaatga gacgttgatc      2460

ggcacgtaag aggttccaac tttcaccata atgaaataag atcactaccg ggcgtatttt     2520

ttgagttatc gagattttca ggagctaagg aagctaaaat ggagaaaaaa atcactggat     2580

ataccaccgt tgatatatcc caatggcatc gtaaagaaca ttttgaggca tttcagtcag     2640
```

```
ttgctcaatg tacctataac cagaccgttc agctggatat tacggccttt ttaaagaccg    2700

taaagaaaaa taagcacaag ttttatccgg cctttattca cattcttgcc cgcctgatga    2760

atgctcatcc ggaattccgt atggcaatga aagacggtga gctggtgata tgggatagtg    2820

ttcacccttg ttacaccgtt ttccatgagc aaactgaaac gttttcatcg ctctggagtg    2880

aataccacga cgatttccgg cagtttctac acatatattc gcaagatgtg gcgtgttacg    2940

gtgaaaacct ggcctatttc cctaaagggt ttattgagaa tatgtttttc gtctcagcca    3000

atccctgggt gagtttcacc agttttgatt taaacgtggc caatatggac aacttcttcg    3060

cccccgtttt caccatgggc aaatattata cgcaaggcga caaggtgctg atgccgctgg    3120

cgattcaggt tcatcatgcc gtctgtgatg gcttccatgt cggcagaatg cttaatgaat    3180

tacaacagta ctgcgatgag tggcagggcg gggcgtaatt tttttaaggc agttattggt    3240

gcccttaaac gcctggtgct acgcctgaat aagtgataat aagcggatga atggcagaaa    3300

ttcgaaagca aattcgaccc ggtcgtcggt tcagggcagg gtcgttaaat agccgcttat    3360

gtctattgct ggtttaccgg tttattgact accggaagca gtgtgaccgt gtgcttctca    3420

aatgcctgag gccagtttgc tcaggctctc cccgtggagg taataattga cgatatgatc    3480

atttattctg cctcccagag cctgataaaa acggttagcg cttcgttaat acagatgtag    3540

gtgttccaca gggtagccag cagcatcctg cgatgcagat ccggaacata atggtgcagg    3600

gcgcttgttt cggcgtgggt atggtggcag gccccgtggc cgggggactg ttgggcgctg    3660

ccggcacctg tcctacgagt tgcatgataa agaagacagt cataagtgcg gcgacgatag    3720

tcatgccccg cgcccaccgg aaggagctac cggacagcgg tgcggactgt tgtaactcag    3780

aataagaaat gaggccgctc atggcgttga ctctcagtca tagtatcgtg gtatcaccgg    3840

ttggttccac tctctgttgc gggcaacttc agcagcacgt aggggacttc cgcgtttcca    3900

gactttacga aacacggaaa ccgaagacca ttcatgttgt tgctcaggtc gcagacgttt    3960

tgcagcagca gtcgcttcac gttcgctcgc gtatcggtga ttcattctgc taaccagtaa    4020

ggcaaccccg ccagcctagc cgggtcctca acgacaggag cacgatcatg cgcacccgtg    4080

gccaggaccc aacgctgccc gagatgcgcc gcgtgcggct gctggagatg cggacgcga    4140

tggatatgtt ctgccaaggg ttggtttgcg cattcacagt tctccgcaag aattgattgg    4200

ctccaattct tggagtggtg aatccgttag cgaggtgccg ccggcttcca ttcaggtcga    4260

ggtggcccgg ctccatgcac cgcgacgcaa cgcggggagg cagacaaggt atagggcggc    4320

gcctacaatc catgccaacc cgttccatgt gctcgccgag cggcataaa  tcgccgtgac    4380
```

```
        gatcagcggt ccagtgatcg aagttaggct ggtaagagcc gcgagcgatc cttgaagctg      4440

        tccctgatgg tcgtcatcta cctgcctgga cagcatggcc tgcaacgcgg gcatcccgat      4500

  5     gccgccggaa gcgagaagaa tcataatggg gaaggccatc cagcctcgcg tcgcgaacgc      4560

        cagcaagacg tagcccagcg cgtcggccgc catgccggcg ataatggcct gcttctcgcc      4620

        gaaacgtttg gtggcgggac cagtgacgaa ggcttgagcg agggcgtgca agattccgaa      4680
  10
        taccgcaagc gacaggccga tcatcgtcgc gctccagcga aagcggtcct cgccgaaaat      4740

        gacccagagc gctgccggca cctgtcctac gagttgcatg ataaagaaga cagtcataag      4800

  15    tgcggcgacg atagtcatgc cccgcgccca ccggaaggag ctgactgggt tgaaggctct      4860

        caagggcatc ggtcgacgct ctcccttatg cgactcctgc attaggaagc agcccagtag      4920

        taggttgagg ccgttgagca ccgccgccgc aaggaatggt gcatgcatcg atcaccacaa      4980
  20
        ttcagcaaat tgtgaacatc atcacgttca tctttccctg gttgccaatg gcccattttc      5040

        ctgtcagtaa cgagaaggtc gcgaattcag gcgcttttta gactggtcgt aatgaacaat      5100

  25    tcttaa                                                                 5106


        <210>   11
        <211>   5597
  30    <212>   DNA
        <213>   Unknown

        <220>
        <223>   Plasmid
  35
        <220>
        <221>   CDS
        <222>   (25)..(1749)
        <223>   scfA - malic enzyme gene
  40

        <400>   11
        aattcttaag aaggagatat acat atg gat att caa aaa aga gtg agt gac            51
                                   Met Asp Ile Gln Lys Arg Val Ser Asp
  45                               1               5

        atg gaa cca aaa aca aaa aaa cag cgt tcg ctt tat atc cct tac gct          99
        Met Glu Pro Lys Thr Lys Lys Gln Arg Ser Leu Tyr Ile Pro Tyr Ala
        10              15                  20                  25
  50
        ggc cct gta ctg ctg gaa ttt ccg ttg ttg aat aaa ggc agt gcc ttc        147
        Gly Pro Val Leu Leu Glu Phe Pro Leu Leu Asn Lys Gly Ser Ala Phe
                        30                  35                  40

  55    agc atg gaa gaa cgc cgt aac ttc aac ctg ctg ggg tta ctg ccg gaa        195
        Ser Met Glu Glu Arg Arg Asn Phe Asn Leu Leu Gly Leu Leu Pro Glu
                        45                  50                  55

        gtg gtc gaa acc atc gaa gaa caa gcg gaa cga gca tgg atc cag tat        243
```

```
             Val Val Glu Thr Ile Glu Glu Gln Ala Glu Arg Ala Trp Ile Gln Tyr
                     60              65              70

      5   cag gga ttc aaa acc gaa atc gac aaa cac atc tac ctg cgt aac atc     291
          Gln Gly Phe Lys Thr Glu Ile Asp Lys His Ile Tyr Leu Arg Asn Ile
                  75              80              85

          cag gac act aac gaa acc ctc ttc tac cgt ctg gta aac aat cat ctt     339
          Gln Asp Thr Asn Glu Thr Leu Phe Tyr Arg Leu Val Asn Asn His Leu
     10   90              95              100             105

          gat gag atg atg cct gtt att tat acc cca acc gtc ggc gca gcc tgt     387
          Asp Glu Met Met Pro Val Ile Tyr Thr Pro Thr Val Gly Ala Ala Cys
                          110             115             120
     15
          gag cgt ttt tct gag atc tac cgc cgt tca cgc ggc gtg ttt atc tct     435
          Glu Arg Phe Ser Glu Ile Tyr Arg Arg Ser Arg Gly Val Phe Ile Ser
                          125             130             135

     20   tac cag aac cgg cac aat atg gac gat att ctg caa aac gtg ccg aac     483
          Tyr Gln Asn Arg His Asn Met Asp Asp Ile Leu Gln Asn Val Pro Asn
                  140             145             150

          cat aat att aaa gtg att gtg gtg act gac ggt gaa cgc att ctg ggg     531
     25   His Asn Ile Lys Val Ile Val Val Thr Asp Gly Glu Arg Ile Leu Gly
                  155             160             165

          ctt ggt gac cag ggc atc ggc ggg atg ggc att ccg atc ggt aaa ctg     579
          Leu Gly Asp Gln Gly Ile Gly Gly Met Gly Ile Pro Ile Gly Lys Leu
     30   170             175             180             185

          tcg ctc tat acc gcc tgt ggc ggc atc agc ccg gcg tat acc ctt ccg     627
          Ser Leu Tyr Thr Ala Cys Gly Gly Ile Ser Pro Ala Tyr Thr Leu Pro
                          190             195             200
     35
          gtg gtg ctg gat gtc gga acg aac aac caa cag ctg ctt aac gat ccg     675
          Val Val Leu Asp Val Gly Thr Asn Asn Gln Gln Leu Leu Asn Asp Pro
                          205             210             215

     40   ctg tat atg ggc tgg cgt aat ccg cgt atc act gac gac gaa tac tat     723
          Leu Tyr Met Gly Trp Arg Asn Pro Arg Ile Thr Asp Asp Glu Tyr Tyr
                          220             225             230

          gaa ttc gtt gat gaa ttt atc cag gct gtg aaa caa cgc tgg cca gac     771
     45   Glu Phe Val Asp Glu Phe Ile Gln Ala Val Lys Gln Arg Trp Pro Asp
                          235             240             245

          gtg ctg ttg cag ttt gaa gac ttt gct caa aaa aat gcg atg ccg tta     819
          Val Leu Leu Gln Phe Glu Asp Phe Ala Gln Lys Asn Ala Met Pro Leu
     50   250             255             260             265

          ctt aac cgc tat cgc aat gaa att tgt tct ttt aac gat gac att cag     867
          Leu Asn Arg Tyr Arg Asn Glu Ile Cys Ser Phe Asn Asp Asp Ile Gln
                          270             275             280
     55
          ggc act gcg gcg gta aca gtc ggc aca ctg atc gca gca agc cgc gcg     915
          Gly Thr Ala Ala Val Thr Val Gly Thr Leu Ile Ala Ala Ser Arg Ala
                          285             290             295
```

```
gca ggt ggt cag tta agc gag aaa aaa atc gtc ttc ctt ggc gca ggt      963
Ala Gly Gly Gln Leu Ser Glu Lys Lys Ile Val Phe Leu Gly Ala Gly
        300                 305                 310

tca gcg gga tgc ggc att gcc gaa atg atc atc tcc cag acc cag cgc     1011
Ser Ala Gly Cys Gly Ile Ala Glu Met Ile Ile Ser Gln Thr Gln Arg
        315                 320                 325

gaa gga tta agc gag gaa gcg gcg cgg cag aaa gtc ttt atg gtc gat     1059
Glu Gly Leu Ser Glu Glu Ala Ala Arg Gln Lys Val Phe Met Val Asp
330                 335                 340                 345

cgc ttt ggc ttg ctg act gac aag atg ccg aac ctg ctg cct ttc cag     1107
Arg Phe Gly Leu Leu Thr Asp Lys Met Pro Asn Leu Leu Pro Phe Gln
                350                 355                 360

acc aaa ctg gtg cag aag cgc gaa aac ctc agt gac tgg gat acc gac     1155
Thr Lys Leu Val Gln Lys Arg Glu Asn Leu Ser Asp Trp Asp Thr Asp
                365                 370                 375

agc gat gtg ctg tca ctg ctg gat gtg gtg cgc aat gta aaa cca gat     1203
Ser Asp Val Leu Ser Leu Leu Asp Val Val Arg Asn Val Lys Pro Asp
                380                 385                 390

att ctg att ggc gtc tca gga cag acc ggg ctg ttt acg gaa gag atc     1251
Ile Leu Ile Gly Val Ser Gly Gln Thr Gly Leu Phe Thr Glu Glu Ile
                395                 400                 405

atc cgt gag atg cat aaa cac tgt ccg cgt ccg atc gtg atg ccg ctg     1299
Ile Arg Glu Met His Lys His Cys Pro Arg Pro Ile Val Met Pro Leu
410                 415                 420                 425

tct aac ccg acg tca cgc gtg gaa gcc aca ccg cag gac att atc gcc     1347
Ser Asn Pro Thr Ser Arg Val Glu Ala Thr Pro Gln Asp Ile Ile Ala
                430                 435                 440

tgg acc gaa ggt aac gcg ctg gtc gcc acg ggc agc ccg ttt aat cca     1395
Trp Thr Glu Gly Asn Ala Leu Val Ala Thr Gly Ser Pro Phe Asn Pro
                445                 450                 455

gtg gta tgg aaa gat aaa atc tac cct atc gcc cag tgt aac aac gcc     1443
Val Val Trp Lys Asp Lys Ile Tyr Pro Ile Ala Gln Cys Asn Asn Ala
                460                 465                 470

ttt att ttc ccg ggc atc ggc ctg ggt gtt att gct tcc ggc gcg tca     1491
Phe Ile Phe Pro Gly Ile Gly Leu Gly Val Ile Ala Ser Gly Ala Ser
                475                 480                 485

cgt atc acc gat gag atg ctg atg tcg gca agt gaa acg ctg gcg cag     1539
Arg Ile Thr Asp Glu Met Leu Met Ser Ala Ser Glu Thr Leu Ala Gln
490                 495                 500                 505

tat tca cca ttg gtg ctg aac ggc gaa ggt atg gta ctg ccg gaa ctg     1587
Tyr Ser Pro Leu Val Leu Asn Gly Glu Gly Met Val Leu Pro Glu Leu
                510                 515                 520

aaa gat att cag aaa gtc tcc cgc gca att gcg ttt gcg gtt ggc aaa     1635
Lys Asp Ile Gln Lys Val Ser Arg Ala Ile Ala Phe Ala Val Gly Lys
                525                 530                 535
```

```
atg gcg cag cag caa ggc gtg gcg gtg aaa acc tct gcc gaa gcc ctg    1683
Met Ala Gln Gln Gln Gly Val Ala Val Lys Thr Ser Ala Glu Ala Leu
        540             545             550

caa cag gcc att gac gat aat ttc tgg caa gcc gaa tac cgc gac tac    1731
Gln Gln Ala Ile Asp Asp Asn Phe Trp Gln Ala Glu Tyr Arg Asp Tyr
        555             560             565

cgc cgt acc tcc atc taa aagcttatcg atgataagct gtcaaacatg          1779
Arg Arg Thr Ser Ile
570

agaattacaa cttatatcgt atggggctga cttcaggtgc tacatttgaa gagataaatt    1839

gcactgaaat ctagaaatat tttatctgat taataagatg atcttcttga gatcgttttg    1899

gtctgcgcgt aatctcttgc tctgaaaacg aaaaaaccgc cttgcagggc ggttttcga     1959

aggttctctg agctaccaac tctttgaacc gaggtaactg gcttggagga gcgcagtcac    2019

caaaacttgt cctttcagtt tagccttaac cggcgcatga cttcaagact aactcctcta    2079

aatcaattac cagtggctgc tgccagtggt gcttttgcat gtctttccgg gttggactca    2139

agacgatagt taccggataa ggcgcagcgg tcggactgaa cggggggttc gtgcatacag    2199

tccagcttgg agcgaactgc ctacccggaa ctgagtgtca ggcgtggaat gagacaaacg    2259

cggccataac agcggaatga caccggtaaa ccgaaaggca ggaacaggag agcgcacgag    2319

ggagccgcca ggggaaacgc ctggtatctt tatagtcctg tcgggtttcg ccaccactga    2379

tttgagcgtc agatttcgtg atgcttgtca gggggcgga gcctatggaa aaacggcttt    2439

gccgcggccc tctcacttcc ctgttaagta tcttcctggc atcttccagg aaatctccgc    2499

cccgttcgta agccatttcc gctcgccgca gtcgaacgac cgagcgtagc gagtcagtga    2559

gcgaggaagc ggaatatatc ctgtatcaca tattctgctg acgcaccggt gcagccttt    2619

ttctcctgcc acatgaagca cttcactgac accctcatca gtgccaacat agtaagccag    2679

tatacactcc gctagcgctg atgtccggcg gtgcttttgc cgttacgcac cacccgtca    2739

gtagctgaac aggagggaca gctgatagaa acagaagcca ctggagcacc tcaaaaacac    2799

catcatacac taaatcagta agttggcagc atcacccgac gcactttgcg ccgaataaat    2859

acctgtgacg gaagatcact tcgcagaata aataaatcct ggtgtccctg ttgataccgg    2919

gaagccctgg gccaactttt ggcgaaaatg agacgttgat cggcacgtaa gaggttccaa    2979

ctttcaccat aatgaaataa gatcactacc gggcgtattt tttgagttat cgagattttc    3039

aggagctaag gaagctaaaa tggagaaaaa aatcactgga tataccaccg ttgatatatc    3099

ccaatggcat cgtaaagaac attttgaggc atttcagtca gttgctcaat gtacctataa    3159
```

```
ccagaccgtt cagctggata ttacggcctt tttaaagacc gtaaagaaaa ataagcacaa   3219

gttttatccg gcctttattc acattcttgc ccgcctgatg aatgctcatc cggaattccg   3279

tatggcaatg aaagacggtg agctggtgat atgggatagt gttcaccctt gttacaccgt   3339

tttccatgag caaactgaaa cgttttcatc gctctggagt gaataccacg acgatttccg   3399

gcagtttcta cacatatatt cgcaagatgt ggcgtgttac ggtgaaaacc tggcctattt   3459

ccctaaaggg tttattgaga atatgttttt cgtctcagcc aatccctggg tgagtttcac   3519

cagttttgat ttaaacgtgg ccaatatgga caacttcttc gcccccgttt tcaccatggg   3579

caaatattat acgcaaggcg acaaggtgct gatgccgctg gcgattcagg ttcatcatgc   3639

cgtctgtgat ggcttccatg tcggcagaat gcttaatgaa ttacaacagt actgcgatga   3699

gtggcagggc ggggcgtaat ttttttaagg cagttattgg tgcccttaaa cgcctggtgc   3759

tacgcctgaa taagtgataa taagcggatg aatggcagaa attcgaaagc aaattcgacc   3819

cggtcgtcgg ttcagggcag ggtcgttaaa tagccgctta tgtctattgc tggtttaccg   3879

gtttattgac taccggaagc agtgtgaccg tgtgcttctc aaatgcctga ggccagtttg   3939

ctcaggctct ccccgtggag gtaataattg acgatatgat catttattct gcctcccaga   3999

gcctgataaa aacggttagc gcttcgttaa tacagatgta ggtgttccac agggtagcca   4059

gcagcatcct gcgatgcaga tccggaacat aatggtgcag ggcgcttgtt cggcgtggg   4119

tatggtggca ggccccgtgg ccgggggact gttgggcgct gccggcacct gtcctacgag   4179

ttgcatgata aagaagacag tcataagtgc ggcgacgata gtcatgcccc gcgcccaccg   4239

gaaggagcta ccggacagcg gtgcggactg ttgtaactca gaataagaaa tgaggccgct   4299

catggcgttg actctcagtc atagtatcgt ggtatcaccg gttggttcca ctctctgttg   4359

cgggcaactt cagcagcacg tagggggactt ccgcgtttcc agactttacg aaacacggaa   4419

accgaagacc attcatgttg ttgctcaggt cgcagacgtt ttgcagcagc agtcgcttca   4479

cgttcgctcg cgtatcggtg attcattctg ctaaccagta aggcaacccc gccagcctag   4539

ccgggtcctc aacgacagga gcacgatcat gcgcacccgt ggccaggacc caacgctgcc   4599

cgagatgcgc cgcgtgcggc tgctggagat ggcggacgcg atggatatgt ctgccaagg   4659

gttggtttgc gcattcacag ttctccgcaa gaattgattg ctccaattc ttggagtggt   4719

gaatccgtta gcgaggtgcc gccggcttcc attcaggtcg aggtggcccg gctccatgca   4779

ccgcgacgca acgcggggag gcagacaagg tatagggcgg cgcctacaat ccatgccaac   4839

ccgttccatg tgctcgccga ggcggcataa atcgccgtga cgatcagcgg tccagtgatc   4899

gaagttaggc tggtaagagc cgcgagcgat ccttgaagct gtccctgatg gtcgtcatct   4959
```

```
acctgcctgg acagcatggc ctgcaacgcg ggcatcccga tgccgccgga agcgagaaga    5019

atcataatgg ggaaggccat ccagcctcgc gtcgcgaacg ccagcaagac gtagcccagc    5079

gcgtcggccg ccatgccggc gataatggcc tgcttctcgc cgaaacgttt ggtggcggga    5139

ccagtgacga aggcttgagc gagggcgtgc aagattccga ataccgcaag cgacaggccg    5199

atcatcgtcg cgctccagcg aaagcggtcc tcgccgaaaa tgacccagag cgctgccggc    5259

acctgtccta cgagttgcat gataaagaag acagtcataa gtgcggcgac gatagtcatg    5319

ccccgcgccc accggaagga gctgactggg ttgaaggctc tcaagggcat cggtcgacgc    5379

tctcccttat gcgactcctg cattaggaag cagcccagta gtaggttgag gccgttgagc    5439

accgccgccg caaggaatgg tgcatgcatc gatcaccaca attcagcaaa ttgtgaacat    5499

catcacgttc atctttccct ggttgccaat ggcccatttt cctgtcagta acgagaaggt    5559

cgcgaattca ggcgcttttt agactggtcg taatgaac                          5597
```

```
<210>    12
<211>    574
<212>    PRT
<213>    Unknown

<220>
<223>    Plasmid

<400>    12
```

```
Met Asp Ile Gln Lys Arg Val Ser Asp Met Glu Pro Lys Thr Lys Lys
1               5                   10                  15

Gln Arg Ser Leu Tyr Ile Pro Tyr Ala Gly Pro Val Leu Leu Glu Phe
            20                  25                  30

Pro Leu Leu Asn Lys Gly Ser Ala Phe Ser Met Glu Glu Arg Arg Asn
        35                  40                  45

Phe Asn Leu Leu Gly Leu Leu Pro Glu Val Val Glu Thr Ile Glu Glu
    50                  55                  60

Gln Ala Glu Arg Ala Trp Ile Gln Tyr Gln Gly Phe Lys Thr Glu Ile
65                  70                  75                  80

Asp Lys His Ile Tyr Leu Arg Asn Ile Gln Asp Thr Asn Glu Thr Leu
                85                  90                  95

Phe Tyr Arg Leu Val Asn Asn His Leu Asp Glu Met Met Pro Val Ile
```

```
                    100                      105                      110

  5    Tyr Thr Pro Thr Val Gly Ala Ala Cys Glu Arg Phe Ser Glu Ile Tyr
               115                 120                 125

 10    Arg Arg Ser Arg Gly Val Phe Ile Ser Tyr Gln Asn Arg His Asn Met
               130                 135                 140

       Asp Asp Ile Leu Gln Asn Val Pro Asn His Asn Ile Lys Val Ile Val
       145                 150                 155                 160
 15
       Val Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly Asp Gln Gly Ile Gly
                       165                 170                 175

 20    Gly Met Gly Ile Pro Ile Gly Lys Leu Ser Leu Tyr Thr Ala Cys Gly
                       180                 185                 190

       Gly Ile Ser Pro Ala Tyr Thr Leu Pro Val Val Leu Asp Val Gly Thr
 25                195                 200                 205

       Asn Asn Gln Gln Leu Leu Asn Asp Pro Leu Tyr Met Gly Trp Arg Asn
               210                 215                 220
 30
       Pro Arg Ile Thr Asp Asp Glu Tyr Tyr Glu Phe Val Asp Glu Phe Ile
       225                 230                 235                 240

 35
       Gln Ala Val Lys Gln Arg Trp Pro Asp Val Leu Leu Gln Phe Glu Asp
                       245                 250                 255

 40    Phe Ala Gln Lys Asn Ala Met Pro Leu Leu Asn Arg Tyr Arg Asn Glu
                       260                 265                 270

       Ile Cys Ser Phe Asn Asp Asp Ile Gln Gly Thr Ala Ala Val Thr Val
 45            275                 280                 285

       Gly Thr Leu Ile Ala Ala Ser Arg Ala Ala Gly Gly Gln Leu Ser Glu
               290                 295                 300
 50
       Lys Lys Ile Val Phe Leu Gly Ala Gly Ser Ala Gly Cys Gly Ile Ala
       305                 310                 315                 320

 55
       Glu Met Ile Ile Ser Gln Thr Gln Arg Glu Gly Leu Ser Glu Glu Ala
                       325                 330                 335
```

```
        Ala Arg Gln Lys Val Phe Met Val Asp Arg Phe Gly Leu Leu Thr Asp
                    340                 345                 350

  5     Lys Met Pro Asn Leu Leu Pro Phe Gln Thr Lys Leu Val Gln Lys Arg
                    355                 360                 365

 10     Glu Asn Leu Ser Asp Trp Asp Thr Asp Ser Asp Val Leu Ser Leu Leu
                    370                 375                 380

        Asp Val Val Arg Asn Val Lys Pro Asp Ile Leu Ile Gly Val Ser Gly
        385                 390                 395                 400
 15

        Gln Thr Gly Leu Phe Thr Glu Glu Ile Ile Arg Glu Met His Lys His
                            405                 410                 415

 20
        Cys Pro Arg Pro Ile Val Met Pro Leu Ser Asn Pro Thr Ser Arg Val
                    420                 425                 430

 25     Glu Ala Thr Pro Gln Asp Ile Ile Ala Trp Thr Glu Gly Asn Ala Leu
                    435                 440                 445

        Val Ala Thr Gly Ser Pro Phe Asn Pro Val Val Trp Lys Asp Lys Ile
 30         450                 455                 460

        Tyr Pro Ile Ala Gln Cys Asn Asn Ala Phe Ile Phe Pro Gly Ile Gly
        465                 470                 475                 480
 35

        Leu Gly Val Ile Ala Ser Gly Ala Ser Arg Ile Thr Asp Glu Met Leu
                            485                 490                 495

 40
        Met Ser Ala Ser Glu Thr Leu Ala Gln Tyr Ser Pro Leu Val Leu Asn
                    500                 505                 510

 45     Gly Glu Gly Met Val Leu Pro Glu Leu Lys Asp Ile Gln Lys Val Ser
                    515                 520                 525

        Arg Ala Ile Ala Phe Ala Val Gly Lys Met Ala Gln Gln Gln Gly Val
 50         530                 535                 540

        Ala Val Lys Thr Ser Ala Glu Ala Leu Gln Gln Ala Ile Asp Asp Asn
        545                 550                 555                 560
 55

        Phe Trp Gln Ala Glu Tyr Arg Asp Tyr Arg Arg Thr Ser Ile
                            565                 570
```

```
        <210>   13
        <211>   5068
        <212>   DNA
  5     <213>   Artificial

        <220>
        <223>   Plasmid

 10     <400>   13
        tatgtatccg gatttaaaag gaaaagtcgt cgctattaca ggagctgctt cagggctcgg      60

        aaaggcgatg gccattcgct tcggcaagga gcaggcaaaa gtggttatca actattatag     120

 15     taataaacaa gatccgaacg aggtaaaaga agaggtcatc aaggcgggcg gtgaagctgt     180

        tgtcgtccaa ggagatgtca cgaaagagga agatgtaaaa aatatcgtgc aaacggcaat     240

        taaggagttc ggcacactcg atattatgat taataatgcc ggtcttgaaa atcctgtgcc     300
 20
        atctcacgaa atgccgctca aggattggga taaagtcatc ggcacgaact taacgggtgc     360

        cttttttagga agccgtgaag cgattaaata tttcgtagaa aacgatatca agggaaatgt     420

 25     cattaacatg tccagtgtgc acgaagtgat tccttggccg ttatttgtcc actatgcggc     480

        aagtaaaggc gggataaagc tgatgacaga acattagcg ttggaatacg cgccgaaggg     540

        cattcgcgtc aataatattg gccaggtgc gatcaacacg ccaatcaatg ctgaaaaatt     600
 30
        cgctgaccct aaacagaaag ctgatgtaga aagcatgatt ccaatgggat atatcggcga     660

        accggaggag atcgccgcag tagcagcctg gcttgcttcg aaggaagcca gctacgtcac     720

 35     aggcatcacg ttattcgcgg acggcggtat gacacaatat ccttcattcc aggcaggccg     780

        cggttaatag tagaagcttc tgttttggcg gatgagagaa gattttcagc ctgatacaga     840

        ttaaatcaga acgcagaagc ggtctgataa aacagaattt gcctggcggc agtagcgcgg     900
 40
        tggtcccacc tgaccccatg ccgaactcag aagtgaaacg ccgtagcgcc gatggtagtg     960

        tggggtctcc ccatgcgaga gtagggaact gccaggcatc aaataaaacg aaaggctcag    1020

 45     tcgaaagact gggcctttcg ttttatctgt tgtttgtcgg tgaacgctct cctgagtagg    1080

        acaaatccgc cgggagcgga tttgaacgtt gcgaagcaac ggcccggagg gtggcgggca    1140

        ggacgcccgc cataaactgc caggcatcaa attaagcaga aggccatcct gacggatggc    1200
 50
        cttttttgcgt ttctacaaac tcttttgttt attttctaa atacattcaa atatgtatcc    1260

        gctcatgaga caataaccct gataaatgct tcaataatat tgaaaaagga agagtatgag    1320

 55     tattcaacat ttccgtgtcg cccttattcc cttttttgcg gcattttgcc ttcctgtttt    1380

        tgctcaccca gaaacgctgg tgaaagtaaa agatgctgaa gatcagttgg gtgcacgagt    1440

        gggttacatc gaactggatc tcaacagcgg taagatcctt gagagttttc gccccgaaga    1500
```

```
acgttttcca atgatgagca cttttaaagt tctgctatgt ggcgcggtat tatcccgtgt    1560

tgacgccggg caagagcaac tcggtcgccg catacactat tctcagaatg acttggttga    1620

gtactcacca gtcacagaaa agcatcttac ggatggcatg acagtaagag aattatgcag    1680

tgctgccata accatgagtg ataacactgc ggccaactta cttctgacaa cgatcggagg    1740

accgaaggag ctaaccgctt ttttgcacaa catgggggat catgtaactc gccttgatcg    1800

ttgggaaccg gagctgaatg aagccatacc aaacgacgag cgtgacacca cgatgcctgt    1860

agcaatggca acaacgttgc gcaaactatt aactggcgaa ctacttactc tagcttcccg    1920

gcaacaatta atagactgga tggaggcgga taaagttgca ggaccacttc tgcgctcggc    1980

ccttccggct ggctggttta ttgctgataa atctggagcc ggtgagcgtg ggtctcgcgg    2040

tatcattgca gcactggggc cagatggtaa gccctcccgt atcgtagtta tctacacgac    2100

ggggagtcag gcaactatgg atgaacgaaa tagacagatc gctgagatag gtgcctcact    2160

gattaagcat tggtaactgt cagaccaagt ttactcatat atactttaga ttgatttaaa    2220

acttcatttt taatttaaaa ggatctaggt gaagatcctt tttgataatc tcatgaccaa    2280

aatcccttaa cgtgagtttt cgttccactg agcgtcagac cccgtagaaa agatcaaagg    2340

atcttcttga tcctttttt ttctgcgcgt aatctgctgc ttgcaaacaa aaaaaccacc    2400

gctaccagcg gtggtttgtt tgccggatca agagctacca actctttttc cgaaggtaac    2460

tggcttcagc agagcgcaga taccaaatac tgtccttcta gtgtagccgt agttaggcca    2520

ccacttcaag aactctgtag caccgcctac atacctcgct ctgctaatcc tgttaccagt    2580

ggctgctgcc agtggcgata agtcgtgtct taccgggttg gactcaagac gatagttacc    2640

ggataaggcg cagcggtcgg gctgaacggg gggttcgtgc acacagccca gcttggagcg    2700

aacgacctac accgaactga gatacctaca gcgtgagcta tgagaaagcg ccacgcttcc    2760

cgaagggaga aaggcggaca ggtatccggt aagcggcagg gtcggaacag gagagcgcac    2820

gagggagctt ccaggggaa acgcctggta tctttatagt cctgtcgggt ttcgccacct    2880

ctgacttgag cgtcgatttt tgtgatgctc gtcagggggg cggagcctat ggaaaaacgc    2940

cagcaacgcg gcctttttac ggttcctggc cttttgctgg ccttttgctc acatgttctt    3000

tcctgcgtta tcccctgatt ctgtggataa ccgtattacc gcctttgagt gagctgatac    3060

cgctcgccgc agccgaacga ccgagcgcag cgagtcagtg agcgaggaag cggaagagcg    3120

cctgatgcgg tattttctcc ttacgcatct gtgcggtatt tcacaccgca tatatggtgc    3180

actctcagta caatctgctc tgatgccgca tagttaagcc agtatacact ccgctatcgc    3240
```

```
tacgtgactg ggtcatggct gcgccccgac acccgccaac acccgctgac gcgccctgac    3300

gggcttgtct gctcccggca tccgcttaca gacaagctgt gaccgtctcc gggagctgca    3360

tgtgtcagag gttttcaccg tcatcaccga aacgcgcgag gcagctgcgg taaagctcat    3420

cagcgtggtc gtgaagcgat tcacagatgt ctgcctgttc atccgcgtcc agctcgttga    3480

gtttctccag aagcgttaat gtctggcttc tgataaagcg ggccatgtta agggcggttt    3540

tttcctgttt ggtcacttga tgcctccgtg taagggggaa tttctgttca tggggggtaat   3600

gataccgatg aaacgagaga ggatgctcac gatacgggtt actgatgatg aacatgcccg    3660

gttactggaa cgttgtgagg gtaaacaact ggcggtatgg atgcggcggg accagagaaa    3720

aatcactcag ggtcaatgcc agcgcttcgt taatacagat gtaggtgttc cacagggtag    3780

ccagcagcat cctgcgatgc agatccggaa cataatggtg cagggcgctg acttccgcgt    3840

ttccagactt tacgaaacac ggaaaccgaa gaccattcat gttgttgctc aggtcgcaga    3900

cgttttgcag cagcagtcgc ttcacgttcg ctcgcgtatc ggtgattcat ctgctaacc     3960

agtaaggcaa ccccgccagc ctagccgggt cctcaacgac aggagcacga tcatgcgcac    4020

ccgtggccag acccaacgc tgcccgagat gcgccgcgtg cggctgctgg agatggcgga     4080

cgcgatggat atgttctgcc aagggttggt ttgcgcattc acagttctcc gcaagaattg    4140

attggctcca attcttggag tggtgaatcc gttagcgagg tgccgccggc ttccattcag    4200

gtcgaggtgg cccggctcca tgcaccgcga cgcaacgcgg ggaggcagac aaggtatagg    4260

gcggcggcgc ctacaatcca tgccaacccg ttccatgtgc tcgccgaggc ggcataaatc    4320

gccgtgacga tcagcggtcc agtgatcgaa gttaggctgg taagagccgc gagcgatcct    4380

tgaagctgtc cctgatggtc gtcatctacc tgcctggaca gcatggcctg caacgcgggc    4440

atcccgatgc cgccggaagc gagaagaatc ataatgggga aggccatcca gcctcgcgtc    4500

gcgaacgcca gcaagacgta gcccagcgcg tcggccgcca tgccggcgat aatggcctgc    4560

ttctcgccga aacgtttggt ggcgggacca gtgacgaagg cttgagcgag ggcgtgcaag    4620

attccgaata ccgcaagcga caggccgatc atcgtcgcgc tccagcgaaa gcggtcctcg    4680

ccgaaaatga cccagagcgc tgccggcacc tgtcctacga gttgcatgat aaagaagaca    4740

gtcataagtg cggcgacgat agtcatgccc cgcgcccacc ggaaggagct gactgggttg    4800

aaggctctca agggcatcgg tcgacgctct cccttatgcg actcctgcat taggaagcag    4860

cccagtagta ggttgaggcc gttgagcacc gccgccgcaa ggaatggtgc atgcatcgat    4920

caccacaatt cagcaaattg tgaacatcat cacgttcatc tttccctggt tgccaatggc    4980

ccattttcct gtcagtaacg agaaggtcgc gaattcaggc gctttttaga ctggtcgtaa    5040
```

```
tgaacaattc ttaagaagga gatataca                                    5068
```